Search for genetic virulence markers in viral haemorrhagic septicaemia virus (VHSV) using a reverse genetics approach

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VHSV is a negative strand RNA virus causing serious disease in farmed rainbow trout. Although VHSV has been eradicated by stamping out procedures in several fresh water bodies, recently including all streams in Denmark, the wildlife marine reservoir still represents a threat against rainbow trout farming. Particularly in Scandinavia, outbreaks of VHS in sea reared rainbow trout have demonstrated that although marine variants of VHSV are considered to be avirulent to rainbow trout, the virus is potentially able to adapt to this host and cause disease. Limited knowledge about the genetic background for virulence to rainbow trout makes it difficult to differentiate between dangerous and harmless VHSV variants. With the aim of identification of genetic virulence markers, we have implemented reverse genetics technology for generation of hybrid virus variants. By substituting different regions in the genome of a virulent VHSV variant with the homologous regions from the genome of an avirulent variant, a set of chimeric viral genomes were generated. Following rescue of the hybrid viruses, the plan is to do comparative challenge experiments in rainbow trout fingerlings in order to assess which substitutions that affect the pathogenicity of the virus.